



ORIGINAL ARTICLE

Evaluation of Bacterial Infections in Bahraini Pediatric Patients From A Tertiary Care Hospital – A Prospective Study

Kasim O. Ardati,^{1*} Soni R. Murdeshwar²

¹Department of Pediatric Infectious Diseases, Bahrain Specialist Hospital, Manama, Kingdom of Bahrain

²Department of Microbiology, Bahrain Specialist Hospital, Manama, Kingdom of Bahrain, P.O.box - 10588

*Corresponding author:

Dr. Kasim O. Ardati, Department of Pediatric Infectious Diseases, Consultant Paediatrician/Pediatric Infectious Diseases, Bahrain Specialist Hospital, Manama, P.O. box -10588, Kingdom of Bahrain, Tel.: (973) 17812000, Email: Kasim@bsh.com.bh

Received date: January 13, 2021; Accepted date: April 8, 2021; Published date: June 30, 2021

Abstract

Background & Objective: Children are prone to a plethora of infections. This study aimed to evaluate the prevalence of most common microorganisms isolated from the bacterial cultures infecting pediatric patients and their resistance to antibiotics in Bahrain.

Methods: This prospective study included 1146 isolates collected from pediatric patients of Bahrain. Demographic details such as age, gender, and nationality were recorded for each of the patients. Samples were cultured using different nutrient media (MacConkey agar, Sheep blood agar etc.), and analysis was done using standard microbiological techniques and Vitex automated analyzer. Application of Kirby-Bauer procedure and Vitex aided in the assessment of antibiotic resistance of the isolates. Proportion test was used to calculate the study outcomes. *P value* < 0.05 was considered statistically significant.

Results: *Streptococcus* group A (52.98%) and *E. coli* (35.97%) were the two most common microorganisms observed in pediatric patients. A high prevalence of Extended-spectrum beta-lactamases (ESBL), *Campylobacter* sp., and Methicillin-resistant *Staphylococcus aureus* (MRSA) were also observed (*P*<0.001). A majority of the organisms were identified from urine (27.66%) and throat cultures (25.22%). *E-coli* showed significant resistance towards trimethoprim /sulfamethoxazole (22.97%) and amoxicillin/ clavulanic acid (20.19%). Susceptibility patterns of gentamicin, amoxicillin, trimethoprim, ciprofloxacin showed significant association with the isolates. Odds of susceptibility of amoxicillin/ clavulanic acid (2.89 times), trimethoprim/sulfamethoxazole (2.29 times) was more for gram-positive isolates but for ciprofloxacin (2.08 times), which was more for gram-negative isolates.

Conclusion: Antimicrobial susceptibility patterns were unique among the pediatric patients of Bahrain.

Keywords: Anti-bacterial Agents, Antimicrobial Stewardship, *Escherichia coli*, Child, Methicillin-Resistant *Staphylococcus aureus*.

Introduction

Children are highly susceptible to a multitude of infections, which are generally mild in nature.^{1,2}

Commonly known infections experienced by the children are gastrointestinal infections, respiratory tract infections, and others. According to a literature

review, it has been observed that the suspected risk factors include daycare attendance, premature birth of the child, duration of breastfeeding, environmental tobacco exposure, contaminated air within the house, and low-socioeconomic status.³

The frequency of such infections varies across age groups. 'Nosocomial infections' (NIs) or hospital-acquired infections, are responsible for causing major threats to the pediatric population, especially to the neonates.⁴ According to the global statistics, around 8.7% of the hospitalized cases suffer from NIs.⁵ Organisms such as gram-negative bacilli, *coagulase-negative Staphylococci*, coagulase-positive *Staphylococci*, *Pseudomonas* spp, and *Streptococcus* sp. are the main causes of NIs whereas the other prevalent bacterial species causing infections are *Staphylococcus aureus*, *Escherichia coli* (*E.coli*), *Proteus mirabilis*, and *Klebsiella pneumoniae*.⁶ During the treatment of these infections, high incidences of antibiotic resistance were observed.⁷ These infections can be managed only through proper surveillance, prevention of transmission, immunization, and counseling.⁸ A study conducted by Salman J et al. (2014) determined the antibiotics surveillance pattern in hospitalized pediatric patients in Bahrain and later distinguished with the European countries.⁹ The study inferred that the prescription of an antibiotic needs to be clinically justified with proper documentation in the case record.⁹ Due to the paucity of literature regarding pediatric bacterial infections and the antimicrobial resistance patterns in Bahrain, the present study assessed the most common microorganisms causing infections in the pediatric population and their antibiotic sensitivity patterns.

Materials and Methods

This was a prospective study conducted at Bahrain specialist hospital for a duration of 5 years (2014 to 2018). Clinical samples such as urine culture, urethral swab, stool samples, eye swabs, and throat swabs received from the patients were labeled using unique hospital numbers; demographic details such as age, gender, and nationality were recorded for each of the patients. Uniqueness in samples was identified based on sample number and culture. Analysis of twenty different cultures

received from the patients was conducted by the Department of Microbiology, Bahrain Specialist Hospital. On culture, different types of bacterial species were obtained, identified, and antibiotic sensitivity was determined.

Procedure

Patient samples were obtained and transferred to the bacteriology laboratory following standard specimen collection and transport protocol. Clinical samples were cultured using different media—MacConkey agar, Sheep blood agar, *Campylobacter* charcoal agar, Selenite broth, *Gardnerella vaginalis* agar, Sabouraud dextrose agar, Thayer Martin agar, Neomycin anaerobic agar, Fluid thioglycollate broth, *Salmonella Shigella* agar, and Chocolate bacitracin agar (Saudi Prepared Media Laboratory Company Ltd, Saudi Arabia). Further, the plates were incubated according to the standard conditions unique to the organisms: 35°C for MacConkey agar, Sabouraud dextrose agar, *Salmonella Shigella* agar, and Mueller Hinton agar whereas, 43°C with 5% CO₂ for *Campylobacter* charcoal agar, 35°C with 5% CO₂ for Sheep blood agar, Chocolate agar, Chocolate bacitracin agar, *Gardnerella vaginalis* agar, and Thayer Martin agar, and 35 °C with 5% CO₂ in anaerobic agar with an anaerobic gas pack for Neomycin anaerobic agar and Sheep blood agar for throat swabs.

Subsequently, the majority of the cultured isolates were identified using Vitex automated analyzer (Vitex® bioMerieux, USA), whereas few isolates were identified manually based on the routine microbiological techniques, such as morphological characteristics on the culture plate, Gram staining, motility test, and biochemical characteristics analysis.¹⁰ Antimicrobial susceptibility profile of each isolate was assessed using disk diffusion method (6-mm disc, OXOID, UK) by Kirby-Bauer procedure and Vitex automated analyzer (Vitex® bioMerieux, USA).¹¹⁻¹³

Vitek GN ID was applied to identify Gram-negative bacilli, Vitek AST N204 was used for sensitivity testing of all Gram-negative bacilli except *Haemophilus influenzae*. For Gram-positive cocci, Vitek ASTGP67 was used except for *Streptococcus* group A, B, C, and G (since they are universally

sensitive to penicillin and cephalosporins only, macrolides were examined by applying Kirby-Bauer method).

Antibiotic sensitivity analysis of the isolates was performed by the Kirby-Bauer method, and the culture-positive patients were divided into three groups, i.e., '0-4', '5-9' and '10-14' years of age.¹⁰⁻¹³

Statistical analysis

Data was analyzed using R i386.3.5.1. and Microsoft Excel. Percentage was applied to calculate the prevalence of organisms over age groups, distribution & pattern of bacterial isolates, and antibiotic resistance in Gram-positive and -negative bacteria. Proportion test was used to calculate the prevalence of different bacterial isolates. And $p < 0.005$ was considered as statistically significant.

Results

A total of 1094 samples and 1146 organisms were received from 976 patients. Based on the age distribution, the majority of the positive culture samples belonged to patients within 5 years of age; female subjects were predominant in the study (533). Extended-spectrum beta-lactamases (ESBL), *Campylobacter* sp. and Methicillin-resistant *Staphylococcus aureus* (MRSA), and others were high under the age group of 0-4 years in both the genders (Table 1). Further, the prevalence of ESBL was significantly more in subjects of age group 0-4 and 5-9 years than the age group "10-14" (p value = 0.0013 and 0.0017, respectively). Also, the prevalence of MRSA was more significant in subjects of age group 0-4 years and 10-14 years than the subjects of age group "5-9" (p = 0.0019 and 0.0068, respectively).

Maximum samples were of urine (27.66%) followed by the throat (25.22%), wound (12.74%), and stool (10.3%) (Table 2). *Streptococcus* group A (26%) and *E. coli* (18.67%) were the chief microorganisms

isolated from pediatric subjects. Gender-wise distribution revealed *Streptococcus* sp. Group A was predominant in males (30.84%), and *E. coli* in females (24.18%), whereas nation-wide distribution showed *Streptococcus* group A (31.05%) and *E. coli* (19.13%) were dominant among samples from Bahrain nationals. Similar observations were noted among the samples obtained from other nationals. (Table 3)

The antibiotic susceptibility analysis for Gram-positive and -negative isolates have been represented in Table 4 (a & b). Specifically, *Streptococcus* Group A demonstrated 13.85% resistance towards erythromycin and 9.18% resistance towards clindamycin; *E. coli* demonstrated major resistance towards trimethoprim /sulfamethoxazole (22.97%) and amoxicillin/clavulanic acid (20.19%). The commonly-tested antibiotics for Gram-positive and -negative groups, susceptibility pattern of gentamicin antibiotic had a significant association with the type of isolate ($p = 0.0001$). The odds of susceptibility of Gram-negative isolates was 2.56 times higher for gentamicin antibiotic than Gram-positive isolates. Further, the susceptibility pattern of amoxicillin/clavulanic acid antibiotic was significantly associated with the type of isolate (p value < 0.0001). The odds of susceptibility of amoxicillin/clavulanic acid antibiotic was 2.89 times more for Gram-positive isolates than the Gram-negative isolates. Similarly, the susceptibility pattern of ciprofloxacin and trimethoprim/sulfamethoxazole antibiotics was significantly associated with the type of isolate (p value 0.0019 and 0.0004, respectively). Odds of susceptibility of ciprofloxacin antibiotic was 2.08 times more for Gram-negative isolates, whereas odds of susceptibility of trimethoprim/sulfamethoxazole was 2.29 times higher for Gram-positive isolates (Table 5 a, b, c).

Table 1: Prevalence of organisms over age group and gender among selected culture positive pediatric patients

Gender	Age group	ESBL (%)	Campylobacter(%)	MRSA (%)	Others (%)	Total samples
Male	0-4 (n=242)	14 (4.79%)	9 (3.08%)	11 (3.77%)	258 (88.36%)	292
	5-9 (n=138)	1 (0.66%)	5 (3.31%)	2 (1.32%)	143 (94.7%)	151
	10-14 (n=63)	0 (0%)	6 (9.09%)	1 (1.52%)	59 (89.39%)	66
Female	0-4 (n=282)	31 (9.06%)	9 (2.63%)	11 (3.22%)	291 (85.09%)	342
	5-9 (n=181)	24 (11.37%)	1 (0.47%)	0 (0%)	186 (88.15%)	211
	10-14 (n=70)	1 (1.19%)	1 (1.19%)	4 (4.76%)	78 (92.86%)	84
Overall	0-4 (n=524)	45 (7.1%)	18 (2.84%)	22 (3.47%)	549 (86.59%)	634
	5-9 (n=319)	25 (6.91%)	6 (1.66%)	2 (0.55%)	329 (90.88%)	362
	10-14 (n=133)	1 (0.67%)	7 (4.67%)	5 (3.33%)	137 (91.33%)	150

ESBL: Extended-spectrum beta-lactamase; MRSA: Methicillin-resistant *Staphylococcus aureus*

*prevalence is calculated among the total samples collected in each age group.

Table 2: Distribution of bacterial isolates in relation to gender, Bahrain, and Non-Bahrain among selected culture positive paediatric patients

Organism name (n)	Male	Female
<i>Escherichia coli</i> (214)	60 (11.79%)	154 (24.18%)
<i>Escherichia coli</i> Extended-spectrum beta-lactamase (ESBL) (71)	15 (2.95%)	56 (8.79%)
<i>Enterobacter aerogenes</i> (6)	2 (0.39%)	4 (0.63%)
<i>Enterobacter cloacae</i> (5)	1 (0.2%)	4 (0.63%)
<i>Klebsiella pneumoniae</i> (35)	11 (2.16%)	24 (3.77%)
Methicillin resistant <i>Staphylococcus aureus</i> (MRSA) (29)	14 (2.75%)	15 (2.35%)
<i>Streptococcus pneumoniae</i> (57)	31 (6.09%)	26 (4.08%)
<i>Proteus mirabilis</i> (48)	21 (4.13%)	27 (4.24%)
<i>Pseudomonas aeruginosa</i> (87)	38 (7.47%)	49 (7.69%)
<i>Salmonella sp.</i> group B (43)	24 (4.72%)	19 (2.98%)
<i>Salmonella sp.</i> group C (14)	5 (0.98%)	9 (1.41%)
<i>Salmonella sp.</i> group D (27)	17 (3.34%)	10 (1.57%)
<i>Salmonella sp.</i> group E or G (5)	3 (0.59%)	2 (0.31%)

<i>Salmonella typhi</i> (3)	1 (0.2%)	2 (0.31%)
<i>Staphylococcus aureus</i> (130)	64 (12.57%)	66 (10.36%)
<i>Streptococcus sp.</i> group A (298)	157 (30.84%)	141 (22.14%)
<i>Streptococcus sp.</i> group B (1)	1 (0.2%)	0 (0%)
<i>Streptococcus sp.</i> group C (9)	5 (0.98%)	4 (0.63%)
<i>Streptococcus sp.</i> group G (22)	13 (2.55%)	9 (1.41%)
<i>Aspergillus</i> (7)	4 (0.79%)	3 (0.47%)
<i>Candida</i> species (4)	2 (0.39%)	2 (0.31%)
<i>Campylobacter</i> species (31)	20 (3.93%)	11 (1.73%)
Total (1146)	509 (44.42%)	637 (55.58%)

Common bacterial isolates among Bahrain and Non-Bahrain culture positive patients

Organism name (n)	Bahrain	Non-Bahrain
<i>Escherichia coli</i> (214)	53 (19.13%)	161 (21.21%)
<i>Escherichia coli</i> ESBL (71)	13 (4.69%)	58 (7.64%)
<i>Enterobacter aerogenes</i> (6)	1 (0.36%)	5 (0.66%)
<i>Enterobacter cloacae</i> (5)	3 (1.08%)	2 (0.26%)
<i>Klebsiella pneumoniae</i> (35)	8 (2.89%)	27 (3.56%)

Methicillin resistant		
<i>Staphylococcus aureus</i> (29)	8 (2.89%)	21 (2.77%)
<i>Streptococcus pneumoniae</i> (34)	9 (3.25%)	25 (3.29%)
<i>Proteus mirabilis</i> (48)	8 (2.89%)	40 (5.27%)
<i>Pseudomonas aeruginosa</i> (87)	28 (10.11%)	59 (7.77%)
<i>Salmonella</i> sp. group B (13)	4 (1.44%)	9 (1.19%)
<i>Salmonella</i> sp. group C (8)	3 (1.08%)	5 (0.66%)
<i>Salmonella</i> sp. group D (12)	4 (1.44%)	8 (1.05%)
<i>Salmonella</i> sp. group E or G (4)	1 (0.36%)	3 (0.4%)
<i>Salmonella typhi</i> (0)	0 (0%)	0 (0%)
<i>Staphylococcus aureus</i> (130)	35 (12.64%)	95 (12.52%)

<i>Streptococcus</i> sp. group A (298)	86 (31.05%)	212 (27.93%)
<i>Streptococcus</i> sp. group B (0)	0 (0%)	0 (0%)
<i>Streptococcus</i> sp. group C (9)	3 (1.08%)	6 (0.79%)
<i>Streptococcus</i> sp. group G (22)	5 (1.81%)	17 (2.24%)
<i>Aspergillus</i> (1)	0 (0%)	1 (0.13%)
<i>Candida</i> species (0)	0 (0%)	0 (0%)
<i>Campylobacter</i> Species (10)	5 (1.81%)	5 (0.66%)
Total (1036)	277 (26.74%)	759 (73.26%)

*multiple samples from same subjects are included.

***110 isolates are excluded in which the nationality is missing.**

Note: 1 and 3 isolates had *Streptococcus* group B and *Salmonella typhi*, but nationality is missing for these samples

Table 3: Pattern of bacteria isolated

	Abcess	Blood	Body Fluid (Includes Gram Stain)	Catheter Tip (Vascular Access)	Genital	Genital Includes Fungal Culture	Hvs	Pharynx	Rule Out Mrsa	Sputum	Stool	Ear Swab	Eye Swab	Nasal Swab	Oral Swab	Rectal Swab	Urethral Swab	Throat	Urine - Uac	Wound (Includes Gram Stain)
<i>Escherichia coli</i> (214)	2 (8.33%)	1 (10%)	3 (15%)	1 (100%)	0 (0%)	1 (33.33%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	2 (2.82%)	1 (1.72%)	2 (4.26%)	0 (0%)	1 (33.33%)	2 (50%)	0 (0%)	170 (53.63%)	28 (19.18%)
<i>Escherichia coli</i> ESBL (71)	2 (8.33%)	0 (0%)	1 (5%)	0 (0%)	1 (50%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	1 (25%)	0 (0%)	57 (17.98%)	9 (6.16%)
<i>Enterobacter aerogenes</i> (6)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	2 (0.63%)	4 (2.74%)
<i>Enterobacter cloacae</i> (5)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	1 (33.33%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	4 (1.26%)	0 (0%)
<i>Klebsiella pneumoniae</i> (35)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	2 (11.76%)	0 (0%)	0 (0%)	0 (0%)	1 (1.41%)	2 (3.45%)	2 (4.26%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	20 (6.31%)	8 (5.48%)
MRSA (29)	8 (33.33%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	1 (5.88%)	2 (66.67%)	0 (0%)	0 (0%)	2 (2.82%)	1 (1.72%)	4 (8.51%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	1 (0.32%)	10 (6.85%)
<i>Streptococcus pneumoniae</i> (57)	0 (0%)	0 (0%)	1 (5%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	1 (5.88%)	0 (0%)	0 (0%)	0 (0%)	9 (12.68%)	33 (56.9%)	13 (27.66%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)
<i>Proteus mirabilis</i> (48)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	1 (33.33%)	1 (33.33%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	1 (33.33%)	0 (0%)	0 (0%)	33 (10.41%)	12 (8.22%)
<i>Pseudomonas aeruginosa</i> (87)	0 (0%)	2 (20%)	3 (15%)	0 (0%)	0 (0%)	0 (0%)	1 (33.33%)	0 (0%)	0 (0%)	2 (40%)	0 (0%)	29 (40.85%)	1 (1.72%)	0 (0%)	1 (20%)	1 (33.33%)	1 (25%)	0 (0%)	23 (7.26%)	23 (15.75%)
<i>Salmonella</i> sp. group B (43)	0 (0%)	1 (10%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	42 (35.59%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)
<i>Salmonella</i> sp. GroupC (14)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	14 (11.86%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)
<i>Salmonella</i> sp. group D (27)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	26 (22.03%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	1 (0.32%)	0 (0%)
<i>Salmonella</i> sp. group E or G (5)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	5 (4.24%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)
<i>Salmonella typhi</i> (3)	0 (0%)	3 (30%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)
<i>Staphylococcus aureus</i> (130)	12 (50%)	1 (10%)	10 (50%)	0 (0%)	0 (0%)	0 (0%)	1 (33.33%)	4 (23.53%)	1 (33.33%)	3 (60%)	0 (0%)	7% (0%)	20% (0%)	24 (51.06%)	3 (60%)	0 (0%)	0 (0%)	0 (0%)	4 (1.26%)	40 (27.4%)
<i>Streptococcus</i> sp. GroupA (298)	0 (0%)	1 (10%)	1 (5%)	0 (0%)	1 (50%)	0 (0%)	0 (0%)	9 (52.94%)	0 (0%)	0 (0%)	0 (0%)	11 (15.49%)	0 (0%)	2 (4.26%)	1 (20%)	0 (0%)	0 (0%)	258 (89.27%)	2 (0.63%)	12 (8.22%)
<i>Streptococcus</i> sp. group B (1)	0 (0%)	1 (10%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)
<i>Streptococcus</i> sp. group C (9)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	9 (3.11%)	0 (0%)	0 (0%)
<i>Streptococcus</i> sp. group G (22)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	22 (7.61%)	0 (0%)	0 (0%)
<i>Aspergillus</i> (7)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	7 (9.86%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)
<i>Candida</i> species (4)	0 (0%)	0 (0%)	1 (5%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	3 (4.23%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)
<i>Campylobacter</i> species (31)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	31 (26.27%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)
Total (1146)	24 (2.09%)	10 (0.87%)	20 (1.75%)	1 (0.09%)	2 (0.17%)	3 (0.26%)	3 (0.26%)	17 (1.48%)	3 (0.26%)	5 (0.44%)	118 (10.3%)	71 (6.2%)	58 (5.06%)	47 (4.1%)	5 (0.44%)	3 (0.26%)	4 (0.35%)	289 (25.22%)	317 (27.66%)	146 (12.74%)

Abbreviations: ESBL:Extended-spectrum beta-lactamase, MRSA:Methicillin-resistant staphylococcus aureus
* Indicates that the Percentage taken from total samples.

Table 4 (a): Antibiotic Resistance pattern of gram-positive bacteria isolated [Number of resistant organism (% of resistance, Total number tested)]

	Ce	CF	Ge	AM	IM	AU	Ox	Pe	Pt	LE	CI	Mxf	ER	VA	CL	LZ	Ts
MRSA (29)	28 (100%,28)	29 (100%, 29)	5 (17.86%, 28)	0 (0%, 11)	-	29 (100%,29)	29 (100%,29)	-	-	12 (50%, 24)	14 (51.85%, 27)	2 (40%,5)	15 (55.56%, 27)	0 (0%,29)	6 (22.22%, 27)	0 (0%, 26)	9 (34.62%,26)
S. pneumoniae (57)	-	0 (0%,57)	30 (71.43%, 42)	-	0 (0%,31)	0 (0%, 53)	9 (32.14%,28)	15 (30%,50)	0 (0%, 10)	0 (0%, 55)	-	-	10 (20.83%, 48)	0 (0%,49)	7 (18.92%, 37)	0 (0%, 12)	1 (2.56%,39)
Streptococcus sp. group A (298)	-	0 (0%,5)	-	-	-	-	-	-	-	-	-	-	41 (13.85%,296)	0 (0%,5)	27 (9.18%, 294)	-	-
Streptococcus sp. group B (1)	0 (0%, 1)	0 (0%, 1)	-	-	-	0 (0%, 1)	-	0 (0%,1)	-	0 (0%,1)	0 (0%, 1)	-	-	0 (0%,1)	1 (100%, 1)	-	0 (0%,1)
Streptococcus sp. group C (9)	-	0 (0%,1)	-	-	-	-	-	-	-	-	-	-	2 (22.22%, 9)	0 (0%,1)	1 (11.11%, 9)	-	-
Streptococcus sp. group G (22)	-	-	-	-	-	-	-	-	-	-	-	-	6 (27.27%, 22)	-	4 (18.18%, 22)	-	-
Staphylococcus aureus (130)	0 (0%, 129)	3 (2.33%,129)	2 (1.65%, 121)	0 (0%, 48)	-	3 (2.33%,129)	0 (0%,129)	-	-	13 (11.5%, 113)	18 (15.13%,119)	-	28 (22.76%,123)	0 (0%,130)	9 (7.44%, 121)	0 (0%, 112)	15 (12.1%,124)
Total (546)	31 (19.62%,158)	32 (14.41%,222)	37 (19.37%,191)	0 (0%, 59)	0 (0%,31)	32 (15.09%,212)	38 (20.43%,186)	15 (29.41%,51)	0 (0%,10)	25 (12.95%,193)	32 (21.77%,147)	2 (40%,5)	102 (19.43%,525)	0 (0%,215)	55 (10.76%,511)	0 (0%, 150)	25 (13.16%,190)

MRSA: Methicillin-resistant Staphylococcus aureus; S. pneumoniae: Streptococcus pneumoniae; Cz: Cefazolin; Ce: Cefuroxime; CF: Ceftriaxone; Ct: Ceftazidime; CM: Cefipime; Ge: Gentamicin; AM: Amikacin; IM: Imipenem; Er: Ertapenem; Au: Augmentin; Ap: Ampicillin; Ox: Oxacillin; Pe: Penicillin; Pt: Piperacillin Tazobactam; LE: Levofloxacin; CI: Ciprofloxacin; Mxf: Moxifloxacin; ER: Erythromycin; VA: Vancomycin; CL: Clindamycin; LZ: Linezolid; Ts: Trimethoprim /Sulfamethoxazole; Me: Meropenem; Cx: Cefixime; Nf: Norfloxacin; Ta: Tazocin

Table 4 (b): Antibiotic Resistance pattern of gram-negative bacteria isolated

	Cz	Ce	Cx	CF	Ct	CM	Ge	AM	IM	Me	Er	AU	Ap	Pt	Le	CI	Nf	Ts
Escherichia coli (214)	5 (2.66%, 188)	3 (1.42%, 211)	2 (0.97%, 206)	1 (0.47%, 212)	1 (0.48%, 209)	2 (2.35%, 85)	2 (2.83%,212)	0 (0%, 196)	0 (0%, 212)	0 (0%, 71)	0 (0%, 48)	43 (20.19%, 213)	-	1 (0.47%,211)	17 (9.55%, 178)	19 (8.92%, 213)	16 (10.81%, 148)	48 (22.97%, 209)
Escherichia coli ESHL (71)	66 (100%, 66)	68 (98.55%, 69)	68 (100%, 68)	68 (98.55%, 69)	68 (98.55%, 69)	54 (98.18%, 55)	27 (38.57%,70)	4 (5.63%, 71)	0 (0%, 70)	0 (0%, 59)	-	65 (92.86%, 70)	-	7 (9.86%, 71)	32 (47.76%, 67)	37 (52.11%, 71)	23 (47.92%, 48)	48 (68.57%, 70)
Enterobacter Aerogenes (6)	6 (100%, 6)	6 (100%, 6)	6 (100%, 6)	0 (0%, 6)	0 (0%, 6)	0 (0%, 4)	0 (0%, 6)	0 (0%, 6)	0 (0%, 6)	0 (0%, 3)	-	6 (100%, 6)	-	0 (0%, 6)	0 (0%, 6)	0 (0%, 6)	0 (0%, 2)	2 (33.33%, 6)
Enterobacter Cloacae (5)	5 (100%, 5)	5 (100%, 5)	5 (100%, 5)	5 (20%, 5)	5 (20%, 5)	0 (0%, 1)	0 (0%, 5)	0 (0%, 5)	0 (0%, 5)	0 (0%, 2)	-	5 (100%, 5)	-	0 (0%, 5)	0 (0%, 5)	0 (0%, 5)	0 (0%, 4)	1 (20%, 5)
Klebsiella Pneumoniae (35)	0 (0%, 26)	0 (0%, 34)	0 (0%, 33)	0 (0%, 34)	0 (0%, 34)	0 (0%, 16)	0 (0%, 35)	0 (0%, 33)	0 (0%, 35)	0 (0%, 15)	-	4 (11.76%, 34)	-	0 (0%, 34)	3 (9.68%, 31)	3 (8.82%, 34)	2 (12.5%, 16)	2 (6.06%, 33)
Proteus Mirabilis (48)	2 (4.65%, 43)	2 (4.17%, 48)	2 (4.35%, 46)	2 (4.17%, 48)	2 (4.35%, 46)	2 (9.09%, 22)	2 (4.17%, 48)	0 (4.44%, 45)	0 (0%, 47)	0 (0%, 20)	0 (0%, 14)	4 (8.33%, 48)	-	0 (0%, 47)	3 (7.89%, 38)	3 (6.38%, 47)	2 (7.41%, 27)	6 (12.77%, 47)
Pseudomonas Aeruginosa (87)	-	-	-	-	2 (2.38%, 84)	1 (2%, 50)	5 (5.75%, 87)	3 (3.45%, 87)	3 (3.45%, 87)	1 (2%, 50)	0 (0%, 16)	-	-	0 (0%, 85)	1 (1.19%, 84)	1 (1.15%, 87)	-	-
Salmonella Group B (43)	-	-	2 (4.76%, 42)	1 (2.38%, 42)	-	-	-	-	-	-	-	10 (23.81%,42)	-	-	-	2 (4.65%, 43)	-	4 (9.52%, 42)
Salmonella Group E or G (5)	-	-	0 (0%, 14)	0 (0%, 14)	-	-	-	-	-	-	-	4 (28.57%,14)	-	-	-	0 (0%, 14)	-	2 (14.29%, 14)
Salmonella Group D (27)	-	-	0 (0%, 26)	0 (0%, 27)	-	-	-	-	-	-	-	11 (40.74%,27)	-	-	-	0 (0%, 27)	-	5 (18.52%, 27)
Salmonella Group C (14)	-	-	0 (0%, 5)	0 (0%, 4)	-	-	-	-	-	-	-	0 (0%, 5)	-	-	-	0 (0%, 5)	-	0 (0%, 5)
Salmonella Typhi (3)	-	-	1 (33.33%, 3)	1 (33.33%, 3)	-	-	-	-	0 (0%, 1)	0 (0%, 1)	0 (0%, 1)	-	2 (66.67%, 3)	1 (100%, 1)	-	1 (33.33%, 3)	-	2 (66.67%, 3)
Aspergillus (7)	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Candida species (4)	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Campylobacter Species(31)	-	0 (0%, 1)	0 (0%, 10)	0 (0%, 10)	-	-	0 (0%, 1)	-	-	-	-	-	4 (36.36%,11)	-	-	1 (9.09%, 11)	-	1 (11.11%, 9)
Total (600)	84 (25.15%, 334)	84 (22.46%, 374)	86 (18.53%, 464)	74 (15.61%, 474)	74 (16.34%, 453)	59 (25.32%, 233)	40 (8.62%,464)	9 (2.03%,443)	3 (0.65%,463)	1 (0.45%,221)	0 (0%, 79)	127 (33.78%, 376)	31 (30.39%,102)	9 (1.96%,460)	56 (13.69%, 409)	67 (11.84%, 566)	43 (17.55%, 245)	121 (25.74%, 470)

Abbreviations: Cz: Cefazolin; Ce: Cefuroxime; CF: Ceftriaxone; Ct: Ceftazidime; CM: Cefipime; Ge: Gentamicin; AM: Amikacin; IM: Imipenem; Er: Ertapenem; Au: Augmentin; Ap: Ampicillin; Ox: Oxacillin; Pe: Penicillin; Pt: Piperacillin Tazobactam; LE: Levofloxacin; CI: Ciprofloxacin; Mxf: Moxifloxacin; ER: Erythromycin; VA: Vancomycin; CL: Clindamycin; LZ: Linezolid; Ts: Trimethoprim /Sulfamethoxazole; Me: Meropenem; Cx: Cefixime; Nf: Norfloxacin; Ta: Tazocin; Az: Azithromycin.

Table 5 (a): Pattern of Pediatric Bacterial Infection and Antibiotic Resistance in Bahrain specialty Hospital Method

	Cefuroxime				Ceftriaxone				Gentamicin				Amikacin			
	S	R	OR [95% CI]	P-value	S	R	OR [95% CI]	P-value	S	R	OR [95% CI]	P-value	S	R	OR [95% CI]	P-value
Gram +	127	31	1.19[0.75,1.88]	0.4672	190	32	1.10[0.70,1.72]	0.682	154	37	0.39[0.24,0.64]	0.0001	59	0	2.49[0.14,43.29]	0.4053 ^{MC}
Gram -	290	84			400	74			424	40			454	9		

^{MC}indicates chi-square test with simulation; Gram +: Gram-positive isolates; Gram -: Gram-negative isolates; S indicates susceptibility; R indicates resistance; OR: Odds ratio; CI: Confidence interval

Table 5 (b): Pattern of Pediatric Bacterial Infection And Antibiotic Resistance in Bahrain’s specialty Hospital Method

	Imipenem				Augmentin				Piperacillin Tazobactam (PT)				Levofloxacin(LF)			
	S	R	OR [95% CI]	P-value	S	R	OR [95% CI]	P-value	S	R	OR [95% CI]	P-value	S	R	OR[95% CI]	P-value
Gram +	31	0	0.48[0.02,9.48]	>0.99 ^{MC}	180	32	2.89[1.88,4.46]	<0.0001	10	0	0.44[0.02,8.10]	>0.99 MC	168	25	1.07[0.64,1.77]	0.8043
Gram -	460	3			247	127			451	9			353	56		

^{MC}indicates chi-square test with simulation; Gram +: Gram-positive isolates; Gram -: Gram-negative isolates; S indicates susceptibility; R indicates resistance; OR: Odds ratio; CI: Confidence interval

Table 5 (c): Pattern of Pediatric Bacterial Infection and Antibiotic Resistance in Bahrain's specialty Hospital Method

	Ciprofloxacin				Trimethoprim/sulfamethoxazole(TS)			
	S	R	OR[95% CI]	P-value	S	R	OR[95% CI]	P-value
Gram +	115	32	0.48[0.30,0.77]	0.0019	165	25	2.29[1.43,3.66]	0.0004
Gram -	499	67			349	121		

Gram +: Gram-positive isolates; Gram - : Gram-negative isolates; S indicates susceptibility; R indicates resistance; OR: Odds ratio; CI: Confidence interval

Discussion

Microbial infections lead to morbidity and mortality in children younger than five years of age. This accounts for about 4 million deaths per year globally.¹⁴ In this study, an increased rate of infection was recorded among children within five years of age. *E. coli* (35.97%) and *Streptococcus* group A (52.98%) were the most common organisms isolated from clinical samples, which can be compared to study conducted in Gulf cooperation countries (GCC) by Mahmoud *et al.* (2012). The study reported prevalence of *E. coli* (44%) at a greater rate followed by *Klebsiella pneumoniae* (20%).¹⁵

The majority of the isolates were collected from urine and throat culture. The predominant organisms obtained from urine culture were *E. coli* (53.63%) followed by *E. coli* ESBL (17.98%), whereas *Streptococcus* sp. Group A (89.27%) was the most common organism from the throat cultures. Several studies have stated that the main causative organism for causing urinary tract infections (UTI) as uropathogenic *E. coli*.¹⁶⁻¹⁸ Study by Tebruegge *et al.* (2011) depicted the data of co-existing meningitis in children <16 years with UTI. The commonest pathogen causing this infection was *E. coli* (67.4%).¹⁹ Similar observations were seen in Saudi Arabia.²⁰

The present research showed a high prevalence of ESBL, *Campylobacter* sp., MRSA under the age group of 0-4 years in both genders. In a five-year study, children of mean age 5.35 years reported how ESBL was the most common bacteria causing UTI, hospitalization, bacterial resistance.²¹ Similarly, Rezai *et al.* (2015) illustrated that 30.5% of isolated *E. coli* was ESBL-producing strain.²² While another study by Roy *et al.* (2017) described a higher prevalence rate of MRSA strains in children under 12 years (63.7%).²³ Also the study

results of Schiaffino *et al.* (2019) were in accordance with the present study findings for *Campylobacter* sp, where the species shows a higher prevalence of phenotypic resistance in children under five years of age.²⁴

While the dominance of *Streptococcus* group A sp. was more in males (31.05%) and *E. coli* in females (24.18%), similar observations were observed in a study conducted by Lin *et al.* where of the total cases, a high proportion of boys were infected with *Streptococcus* group A sp (1.29:1) whereas, in Patwardhan *et al.* study, *E. coli* was more prevalent in girls (74.1%).^{25,26} The current research is one of its kind, as several gram-positive and gram-negative bacteria were isolated from different cultures, fluids, stains, swabs, etc. Urine and throat cultures were maximum in number, indicating the presence of opportunistic organisms. However, there are numerous studies that show the intake of different cultures depending on the symptoms of bacterial infection which can lead to ignorance of other underlying infections/causes of diseases.^{21,27-29}

Gram-positive isolates were highly susceptible to amoxicillin and trimethoprim/sulfamethoxazole, whereas Gram-negative isolates were more susceptible to gentamicin and ciprofloxacin, which is unique in this study. This pioneer study was conducted among the Bahrain population and has added valuable insights to the susceptibility patterns of the organisms infecting some of the Bahraini nationals. But *E. coli* being a gram-negative organism, demonstrated major resistance towards trimethoprim/sulfamethoxazole (22.97%) and amoxicillin (20.19%). A study by Mohammed, reported similar results for gram-negative organisms having a lower susceptibility rate towards antibiotics like ampicillin, amoxicillin-clavulanic acid.³⁰ *Streptococcus* Group A demonstrated 13.85% resistance towards erythromycin and

9.18% resistance towards clindamycin which is partly similar to a study conducted in school children, where 48% of isolates were unsusceptible to erythromycin while none were for clindamycin.³¹

The study has its share of limitations, such as the assessment was conducted at a single hospital. Future studies could involve hospitals across Bahrain in order to obtain a comprehensive picture. Education and awareness among Clinical practitioners and parents are quintessential. Antimicrobial stewardship program is one such program that requires Practitioners to follow evidence-based prescriptions to safeguard the patient's welfare.³²

Conclusion

Frequency and antimicrobial resistance patterns were reported for the first time in a pediatric population. Spanning over five years in Bahrain. The pattern of susceptibility demonstrated by the detected organisms was also unique as compared to reports from the GCC countries.

Further, the prevalence of bacterial infection and antimicrobial resistance can be controlled by the introduction of strong infection control programs and the usage of antimicrobials only on the Clinician's prescription. Additionally, the role of clinical/hospital pharmacists cannot be underestimated in educating children and their parents/guardians.

Funding Sources

Nil

Conflict of interest

None declared

Acknowledgment

Nil

References

1. Bianconi E, Piovesan A, Facchin F, *et al.* An estimation of the number of cells in the human body. *Ann Hum Biol.* 2013;40:463-71.
2. Sender R, Fuchs S, Milo R. Revised estimates for the number of human and bacteria cells in the body. *PLoS Biol.* 2016;14:e1002533.
3. Ohalet C, Ohalet. Bacteriology of different wound infection and their antimicrobial susceptibility patterns in Imo state Nigeria. *World J Pharm Sci.* 2012;13:1155-72.
4. Ford-Jones EL, Mindorff CM, Langley JM, *et al.* Epidemiologic study of 4684 hospital-acquired infections in pediatric patients. *Pediatr Infect Dis J.* 1989;8: 668-75.
5. Bryce J, Boschi-Pinto C, Shibuya K, *et al.* The WHO Child Health Epidemiology Reference Group. WHO Estimates of the Causes of Death in Children? *Lancet.* 2005;365:1147-52.
6. Cleven BE, Palka-Santini M, Gielen J, *et al.* Identification and characterization of bacterial pathogens causing bloodstream infections by DNA microarray. *J Clin Microbiol.* 2006;44: 2389-97.
7. Nikaido H. Multidrug resistance in bacteria. *Annu Rev Biochem.* 2009;78:119-46.
8. Mulu F, Moges, B, Tessema, *et al.* pattern and multiple drug resistance of bacterial pathogens isolated from wound infection at University of Gondar Teaching Hospital, northwest Ethiopia. *Ethiop Med J.* 2006; 44:125-131.
9. Salman. J, Rawan A. Antibiotics Surveillance in Pediatrics In-Patients, a Point Prevalence Comparative Study between Kingdom of Bahrain and the European Union. *Bahrain Medical Bulletin.* 2014; 36:20-24.
10. Trojan R, Razdan L, Singh N. Antibiotic susceptibility patterns of bacterial isolates from pus Samples in a Tertiary Care Hospital of Punjab, India. *Int J Microbiol.* 2016; 2016: 9302692.
11. Shetty N, Hill G, Ridgway GL. The Vitek analyser for routine bacterial identification and susceptibility testing: protocols, problems, and pitfalls. *J Clin Pathol.* 1998;51:316-23.
12. Bauer AW, Kirby WM, Sherris JC, *et al.* Antibiotic susceptibility testing by a standardized single disk method. *Am J Clin Pathol.* 1966;45:493-6.
13. Performance Standards for Antimicrobial Susceptibility Testing, 30th ed. Wayne, Pennsylvania 19087 USA;2020: 1-332
14. Children: Improving Survival And Well-Being.

Available at: <https://www.who.int/news-room/fact-sheets/detail/children-reducing-mortality>. Accessed on 4 November 2020.

15. Aly M, Balkhy HH. The prevalence of antimicrobial resistance in clinical isolates from Gulf Corporation Council countries. *Antimicrob Resist Infect Control*. 2012;19;1:26.
16. Flores-Mireles AL, Walker JN, Caparon M, *et al*. Urinary tract infections: epidemiology, mechanisms of infection and treatment options. *Nat Rev Microbiol*. 2015;13:269-84.
17. Foxman B. Urinary tract infection syndromes: occurrence, recurrence, bacteriology, risk factors, and disease burden. *Infect Dis Clin*. 2014;28;1-13.
18. Foxman B. The epidemiology of urinary tract infection. *Nature Rev Urol*. 2010;7:653-660.
19. Tebruegge M, Pantazidou A, Clifford V, *et al*. The Age-Related Risk of Co-Existing Meningitis in Children with Urinary Tract Infection. *PLoS ONE*. 2011;6:e26576.
20. Zeyaulah M, Kaul V. Prevalence of urinary tract infection and antibiotic resistance pattern in Saudi Arabia population. *G.J.B.A.H.S*. 2015;4:2016-214.
21. Będzichowska A, Przekora J, Stapińska-Syniec A, *et al*. Frequency of infections caused by ESBL-producing bacteria in a pediatric ward - single-center five-year observation. *Arch Med Sci*. 2019;15:688-93.
22. Rezai MS, Salehifar E, Rafiei A, *et al*. Characterization of Multidrug Resistant Extended-Spectrum Beta-Lactamase-Producing *Escherichia coli* among Uropathogens of Pediatrics in North of Iran. *BioMed Res Int*. 2015; 2015:1-7.
23. Roy MP, Gaiind R, Aggarwal KC, *et al*. Pattern of Pediatric Bacterial Infection and Antibiotic Resistance in New Delhi. *Indian Pediatr*. 2017;54:153-54.
24. Schiaffino F, Colston JM, ParedesOlortegui M, *et al*. Antibiotic resistance of *Campylobacter* species in a pediatric cohort study. *Antimicrob Agents Chemother*. 2019;63:e01911-18.
25. Lin MH, Chang PF, Fong WK, *et al*. Epidemiological and clinical features of group A *Streptococcus* pharyngitis in children. *Acta Paediatr Taiwan*. 2003;44:274-278.
26. Patwardhan V, Kumar D, Goel V, *et al*. Changing prevalence and antibiotic drug resistance pattern of pathogens seen in community-acquired pediatric urinary tract infections at a tertiary care hospital of North India. *J Lab Physicians*. 2017;9:264-68.
27. Judith M, Simonian A, Muniz G, *et al*. Comparison of Bacterial Culture Results Obtained from Nasopharyngeal and Midturbinate Swabs in Children With Upper Respiratory Tract Infection Symptoms. *Pediatric Infect Dis J*. 2018; 37:e275-e277.
28. Thornton HV, Hay AD, Redmond NM, *et al*. Throat swabs in children with respiratory tract infection: associations with clinical presentation and potential targets for point-of-care testing. *Fam Pract*. 2017;34:407-15.
29. Catania S, Mascellino MT, Ajassa C, *et al*. Incidence of bacterial colonization in the throat and in urines at paediatric age with evaluation of sensitivity to common antibiotics. *Riv Eur Sci Med Farmacol*. 1996;18:169-172.
30. Mohammad A. Antimicrobial susceptibility of *Escherichia coli* Isolates from Clinical Specimens in Children over a 5-Year Period in Jordan. *Biomed Pharmacol J*. 2016;9.
31. Martin JM, Green M, Barbadora KA, *et al*. Erythromycin-resistant group A streptococci in schoolchildren in Pittsburgh. *N Engl J Med*. 2002; 346:1200-06.
32. Doron S, Davidson LE. Antimicrobial stewardship. *Mayo Clin Proc*. 2011;86:1113-23.